

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

On nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; Search time 1794.5 Seconds
(without alignments) 90.255 Million cell updates/sec

Title: US-09-761-116-1

perfect score: 12

Sequence: 1 gctctgggg 12

Scoring table: IDENTITY_NUC

Gapov 10.0, Gapext 1.0

Post-processing: Minimum Match 0%

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_estbun:*

3: em_estin:*

4: em_estml:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_gss:*

13: em_gss_hum:*

14: em_gss_inv:*

15: em_gss_pln:*

16: em_gss_vrt:*

total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

ALIGNMENTS

Searched: 13736207 seqs, 6748477542 residues

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Gapov 10.0, Gapext 1.0

Post-processing: Minimum Match 0%

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2: em_estbun:*

3: em_estin:*

4: em_estml:*

5: em_estov:*

BASE COUNT	24 a	51 c	33 g	16 t
ORIGIN				
Query Match	100.0%	Score 12; DB 10; Length 124;		
Best Local Similarity	100.0%	Pred. No. 8.6e+03; Mismatches 0;		
Matches	12;	Conservative 0; Indels 0; Gaps 0;		
OY	1 ggcctgggg 12			
Db	21 GCCTCTGGGG 32			
RESULT	7			
AT1712861/c				
LOCUS				
DEFINITION	125 bp mRNA	linear EST 08-JUN-1999		
UTR-AGI-aaf-d-03-0-UI.s2	UT-R-AGI	Rattus norvegicus cDNA clone		
ACCESSION	AT1712861	3', mRNA sequence.		
VERSION	AT1712861.1	GI:5016661		
SOURCE				
ORGANISM	Rattus norvegicus			
EST.	Norway rat.			
JOURNAL				
MEDLINE				
COMMENT				
97044477				
Contact: Soares, MB				
Program for Rat Gene Discovery and Mapping				
University of Iowa				
451 Echstein Medical Research Building Iowa City, IA 52242, USA				
Tel: 319 335 8250				
Fax: 319 335 9565				
Email: msoares@blue.weag.uiowa.edu				
The sequence contained an oligo-dT track that was present in the				
oligonucleotide that was used to prime the synthesis of first				
strand cDNA and therefore this may represent a bona fide poly A				
tail. The sequence tag present in the cDNA between the NotI site				
and the oligo-dT track served to verify it as a clone from the				
normalized ventricle at 13 dpc library cDNA Library Preparation:				
M.B. Soares Lab Clone distribution: clones will be available				
through Research Genetics (www.resgen.com)				
Seq primer: M13 Forward				
POLYA-Yes.				
FEATURES				
source				
1. -125				
/organism="Rattus norvegicus"				
/strain="Sprague-Dawley"				
/db_xref="taxon:10116"				
/clone="UT-R-AGI-aaf-d-0-UI"				
/clone="lib=UT-R-AGI"				
/dev_stage="adult"				
/lab_host="DH10B (Life Technologies)"				
/note="Vector: pMT-Pac (Pharmacia) with a modified				
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AGI				
library is a normalized library constructed from 13 dpc				
rat ventricle. The tag is a string of 6 nucleotides				
present between the Not I site and the oligo-dT track.				
The library was constructed as described by Bonaldo,				
Lennon and Soares, Genome Research 6: 791-805, 1995.				
University of Iowa.				
TAG_LIB=UT-R-AGI				
TAG_SEQ="CAGCGA"				
TAG_SEQ="ventricle at 13 dpc				
BASE COUNT	21 a	31 c	35 g	41 t
ORIGIN				
Query Match	100.0%	Score 12; DB 10; Length 128;		
Best Local Similarity	100.0%	Pred. No. 8.6e+03; Mismatches 0;		
Matches	12;	Conservative 0; Indels 0; Gaps 0;		
OY	1 ggcctgggg 12			
Db	78 GCCTCTGGGG 89			

RESULT	9								
U2587/c									
LOCUS	U25887	129 bp	mRNA	linear	EST 03-Oct-1995				
DEFINITION	HS25887	Human chromosome 12p cDNAs	Homo sapiens	cDNA clone ha4,					
ACCESSION	U25887								
VERSION	U25887.1								
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	1								
AUTHORS	Baens, M., Aerssens, J., van Zand, K., Cassiman, J.J., Van Den Berghe, H., and Marynen, P.								
TITLE	Isolation and regional assignment of chromosome 12p cDNAs								
JOURNAL	Genomics 29 (1), 44-52 (1995)								
MEDLINE	96079090								
COMMENT	Contact: Peter Marynen, Center for Human Genetics, KU Leuven, Herestraat 49, Leuven, B3000, Belgium.								
FEATURES	source								
	1. .129								
	/organism="Homo sapiens"								
	/db_xref="taxon:9606"								
	/map="12p"								
	/clone="hsa4"								
	/clone_id="Human chromosome 12p cDNAs"								
BASIC COUNT	38 a	26 c	22 g	43 t					
ORIGIN									
RESULT	10								
AW520497/c									
LOCUS	AW520497	130 bp	mRNA	linear	EST 06-MAR-2000				
DEFINITION	UT-R-BJOP-afx-b-09-0-UI-s1-UI-R-BJOP	Rattus norvegicus	cDNA clone						
	UT-R-BJOP-afx-b-09-0-UI 3'	mRNA sequence.							
ACCESSION	AW520497								
VERSION	AW520497.1								
KEYWORDS	EST.								
SOURCE	Rattus norvegicus								
ORGANISM	Rattus norvegicus								
REFERENCE	1 (bases 1 to 130)								
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.								
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery								
JOURNAL	Genome Res. 6 (9), 791-806 (1996)								
MEDLINE	9704477								
COMMENT	Contact: Soares, M.B. Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: mssoares@blue.weeg.uiowa.edu								
	The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized Av canal at 16.5 dpc library cDNA Library Preparation:								

RESULT	11								
AQ527525/c									
LOCUS	AQ527525	133 bp	DNA	linear	GSS 18-MAY-1999				
DEFINITION	RPCI-11-366N14.TJ	RPCI-11	Homo sapiens	genomic clone	RPCI-11-366N14				
	, DNA sequence.								
ACCESSION	AQ527525								
VERSION	AQ527525.1								
KEYWORDS	GSS.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	1 (bases 1 to 133)								
AUTHORS	Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.								
TITLE	use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building								
JOURNAL	Unpublished (1997)								
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Bacterial Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: huet@tigr.org								

M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 95-1129, >(GGGA) n#Simple_repeat Seq primer: M13 Forward POLY=A Yes.

FEATURES source

1. .130

location/Qualifiers

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/ab_xref="taxon:0116"

/clone="UI-R-BJOP"

/clone_id="adult"

/dev_stage="adult"

/lab_host="B110B (Life Technologies)"

/note="vector: pRT3D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AAI, UI-R-AB1, UI-R-AC1, UI-R-AD1, UI-R-AEL, UI-R-AFL, and UI-R-AG1 Libraries. These libraries represent tissues from rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc. AV canal at 15 dpc, and ventricle at 13 dpc. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996.

TAG_LIB=UI-R-BJOP

TAG_TISSUE=AV canal at 16.5 dpc

TAG_SEQ=GAACG"

BASE COUNT

29 a

26 c

41 g

34 t

ORIGIN

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

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100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

DB 9;

Length 130;

Best Local Similarity

100.0%

Pred. No. 8.7e+03;

Matches 12;

Indels 0;

Gaps 0;

Qy 1

gcctctggag 12

Db 51

GCCTCTGGAG 40

RESULT

11

Query Match

100.0%

Score 12;

<p

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends

FEATURES
source
location/Qualifiers
1..133

/organism="Homo sapiens"
/db_xref="GDB:760485"
/db_xref="Taxon:9606"
/clone="RPCI-11-366N14"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: PBACE3 6; site_1: ECOLI; site_2: ECOLI;
RPCI-11 Human Male BAC Library"
BASE COUNT
31 a 43 c
ORIGIN
31 a 28 g 31 t

Query Match
Best Local Similarity 100.0%; Score 12; DB 12; Length 133;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcctctggggag 12
Db 92 GCCTCTGGGGAG 81

RESULT 12

BF83463
LOCUS BFB36463 135 bp mRNA linear EST 13-JAN-2001
DEFINITION RC3-HT0974-171100-012-c02 HT0974 Homo sapiens cDNA, mRNA sequence.
ACCESSION BFB36463
VERSION BFB36463.1
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Locus 1 (bases 1 to 136)
AUTHORS Dias Neto, E; Garcia Correa, R.; Verjovski-Almeida, S.; Briones, M. R.,
Nagi, M. A.; da Silva, W. Jr.; Zago, M. A.; Bordin, S.; Costa, F. F.,
Goldman, G. H.; Carvalho, A. F.; Matukuma, A.; Bafia, G. S.; Simpson, D. H.,
Brunstein, A.; de Oliveira, P. S.; Bucher, P.; Jongeneel, C. V.; O'Hare
, M. J.; Soares, F.; Brentani, R. R.; Reis, L. F.; de Souza, S. J. and
Simpson, A. J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
SEQUENCE TAGS sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 2022663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.p1?ti=RC3&t2=RC3-HT0974-171100-012-c02&t3=2000-11-17&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 134.

FEATURES
source
location/Qualifiers

1..135

/organism="Homo sapiens"
/db_xref="Taxon:9606"
/clone_lib="HT0974"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; site_1: SmaI;
site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT
35 a
ORIGIN
33 c 33 c 40 g 28 t

Query Match
Best Local Similarity 100.0%; Score 12; DB 10; Length 136;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcctctggggag 12
Db 81 GCCTCTGGGGAG 92

RESULT 13

AA955315
LOCUS AA955315
DEFINITION UI-R-Al-ew-d-02-0-UI-S1 UI-R-Al Rattus norvegicus cDNA clone
ACCESSION AA955315
VERSION AA955315.1
KEYWORDS EST
ORGANISM Rattus norvegicus
SOURCE Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurogathi; Muridae; Murinae;
Rattus 1 (bases 1 to 138)
AUTHORS Bonaldo, M. F.; Lennon, G. and Soares, M. B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 9704477
COMMENT On May 7, 1998 this sequence version replaced 91:3118899.
Contact: Soares, M.B.
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu

The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult heart library. cDNA Library Preparation: M. Falima Bonaldo,
Ph.D. Clone distribution: clones will be available through the Ludwig Research
Genetics. This clone is also available through the I.M.A.G.E. Consortium at LBL (info@image.llnl.gov). IMAGE ID=177912. The
following repetitive elements were found in this cDNA sequence:
95-129, >(GGGA)n\$Simple_repeat
Seq primer: M13 Forward
POLY-A No.

FEATURES
source
location/Qualifiers
1..138

/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="Taxon:10116"
/clone="UI-R-Al-ew-d-02-0-UI"
/clone.lib="UI-R-Al"
/dev_stage="adult"
/lab.host="DH10B (Life Technologies)"
/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Al
library is a subtracted library derived from the UI-R-Al
library. The UI-R-Al library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present in the vector. The Not I site and the
oligo-dT track which allows identification of the library
of origin or a clone within the mixture. The subtracted

library (UI-R-A1) was constructed as follows: PCR amplified cDNA inserts from a pool of approximately 3,840 UI-R-A0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-A0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-A1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 32 a 28 c 44 g 34 t
ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gcctctgggg 12
Db 51 GGCCTCTGGGG 40

RESULT 14
BE151130/c
LOCUS BE151130 139 bp mRNA linear EST 21-JUN-2000
DEFINITION RC4-HT0277-160200-013-h05
ACCESSION BE151130
VERSION BE151130.1 GI:8613851
VERSION EST:
KEYWORDS human.
ORGANISM Homo sapiens

RESULT 15
AA980863
LOCUS AA980863 146 bp mRNA linear EST 27-MAY-1998
DEFINITION ua46el0.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1349802 5', mRNA sequence.
ACCESSION AA980863
VERSION AA980863.1 GI:3159399
KEYWORDS EST:
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 139)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

COMMENT: Unpublished (1996).
TITLE Contact: Marra M/Mouse EST Project
JOURNAL Washington-HHMI Mouse EST Project
MEDLINE 20202663
TITLE shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
CONTACT: Simpson A.J.G.
COMMENT: Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/qgethtml2.pl?tl=6t2=RC4-HT0277-160
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 139.
Location/Qualifiers

FEATURES source
COMMENT: This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/qgethtml2.pl?tl=6t2=RC4-HT0277-160
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 139.
Location/Qualifiers

FEATURES source
COMMENT: This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/qgethtml2.pl?tl=6t2=RC4-HT0277-160
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 139.
Location/Qualifiers

tissue mRNA and cDNA amplification were performed under low stringency conditions." UI-R-A0 clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UI-R-A0 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-A1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996).

BASE COUNT 30 a 45 c 25 g 39 t
ORIGIN

Query Match 100.0%; Score 12; DB 9; Length 139;
Best Local Similarity 100.0%; Pred. No. 8.8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gcctctgggg 12
Db 43 GGCCTCTGGGG 32

RESULT 15
AA980863
LOCUS AA980863 146 bp mRNA linear EST 27-MAY-1998
DEFINITION ua46el0.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:1349802 5', mRNA sequence.
ACCESSION AA980863
VERSION AA980863.1 GI:3159399
KEYWORDS EST:
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 146)
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubroque, T., Geissel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheibenbogen, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterson, R.
COMMENT: The Washington-HHMI Mouse EST Project
TITLE Unpublished (1996).
JOURNAL Contact: Marra M/Mouse EST Project
MEDLINE Washington-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LInL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
MGI: 693894
Seq primer: -28mm13 rev2 ET from Amersham
High quality sequence stop: 111.
Location/Qualifiers

FEATURES source
COMMENT: This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/qgethtml2.pl?tl=6t2=RC4-HT0277-160
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 139.
Location/Qualifiers

FEATURES source
COMMENT: This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/qgethtml2.pl?tl=6t2=RC4-HT0277-160
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 139.
Location/Qualifiers

Mon May 13 08:58:01 2002

us-09-761-116-1.rst

Page 8

Query Match 100.0%; Score 12; DB 9; Length 146;
Local Similarity 100.0%; Pred. No. 8.9e+03; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gctctgggg 12
|||||||
Db 29 GCTCTGGGG 40

Search completed: May 10, 2002, 16:46:03
Job time: 8833 sec

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on : May 10, 2002, 14:18:50 ; Search time 1906.21 Seconds (without alignments)

Scoring table: IDENTITY_NUC

Perfect score: US-09-761-116-1

Sequence: Gapop 10.0 , Gapext 1.0

Searched: 197656 seqs, 10463261293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : GenEmpl: *

1: gb_ba: *

2: gb_htg: *

3: gb_in: *

4: gb_on: *

5: gb_ov: *

6: gb_pat: *

7: gb_Ph: *

8: gb_Pl: *

9: gb_pr: *

10: gb_ro: *

11: gb_sts: *

12: gb_sy: *

13: gb_un: *

14: gb_vl: *

15: em_ba: *

16: em_fun: *

17: em_hum: *

18: em_in: *

19: em_on: *

20: em_or: *

21: em_ov: *

22: em_Pat: *

23: em_ph: *

24: em_Pl: *

25: em_ro: *

26: em_sts: *

27: em_un: *

28: em_1: *

29: em_mu: *

30: em_htg_hum: *

31: em_htg_inv: *

32: em_htg_other: *

33: em_htg_inv: *

RESULT 1

AR137925 LOCUS ARI137925 12 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 1 from patent US 6197580.

ACCESSION ARI137925

VERSION AR137925.1 GI:14479434

KEYWORDS SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE I (bases 1 to 12)

AUTHORS Susicic,V.S. and Duzic,E.

TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor

ALIGNMENTS

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
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Qy	1	gcctctgggg 12	DEFINITION	Sequence 47 from patent US 6197580.
Db	1	GCCTCTGGGG 12	ACCESSION	AR137971
RESULT	2		VERSION	AR137971.1 GI:14479480
AR137965			KEYWORDS	
LOCUS	AR137965	Sequence 41 from patent US 6197580.	SOURCE	Unknown.
DEFINITION		28 bp DNA	ORGANISM	Unclassified.
ACCESSION	AR137965	linear	REFERENCE	1. (bases 1 to 28)
VERSION	AR137965.1	PAT 16-JUN-2001	AUTHORS	Susulic,V.S. and Duzic,E.
KEYWORDS		JOURNAL	TITLE	Transcriptional regulation of the human .beta.3-adrenergic receptor gene
SOURCE	Unknown.	FEATURES	Patent: US 6197580-A 47 06-MAR-2001;	
ORGANISM	Unclassified.	source	Location/Qualifiers	1. .28
REFERENCE	1. (bases 1 to 28)	BASE COUNT	/organism="unknown"	6 a 9 c 9 g 4 t
AUTHORS	Susulic,V.S. and Duzic,E.	ORIGIN		
TITLE	Transcriptional regulation of the human .beta.3-adrenergic receptor gene			
JOURNAL	Patent: US 6197580-A 41 06-MAR-2001;			
FEATURES	Location/Qualifiers			
SOURCE	1. .28			
BASE COUNT	4 a 10 c 8 g 6 t			
ORIGIN				
RESULT	3		RESULT	5
AR137970			AR137972	
LOCUS	AR137970	Score 12; DB 6; Length 28;	LOCUS	AR137972
DEFINITION	Sequence 46 from patent US 6197580.	Score 12; DB 6; Length 28;	DEFINITION	Sequence 48 from patent US 6197580.
ACCESSION	AR137970	linear	ACCESSION	AR137972
VERSION	AR137970.1	PAT 16-JUN-2001	VERSION	AR137972.1 GI:14479481
KEYWORDS		JOURNAL	KEYWORDS	
SOURCE	Unknown.	FEATURES	SOURCE	Unknown.
ORGANISM	Unclassified.	BASE COUNT	/organism="unknown"	5 a 7 c 11 g 5 t
REFERENCE	1. (bases 1 to 28)	ORIGIN		
AUTHORS	Susulic,V.S. and Duzic,E.			
TITLE	Transcriptional regulation of the human .beta.3-adrenergic receptor gene			
JOURNAL	Patent: US 6197580-A 48 06-MAR-2001;			
FEATURES	Location/Qualifiers			
SOURCE	1. .28			
BASE COUNT	5 a 7 c 11 g 5 t			
ORIGIN				
RESULT	6		RESULT	6
HSU03947			HSU03947	
LOCUS	HSU03947	Score 12; DB 6; Length 28;	LOCUS	HSU03947
DEFINITION	Human MHC class I antigen HLA-C gene (HLA-Cw*0401 allele), intron 1.	Score 12; DB 6; Length 28;	DEFINITION	Human MHC class I antigen HLA-C gene (HLA-Cw*0401 allele), intron 1.
ACCESSION	U39347	linear	ACCESSION	U39347
VERSION	U39347.1	PAT 21-MAR-1997	VERSION	U39347.1 GI:1654171
KEYWORDS		JOURNAL	KEYWORDS	
SOURCE	human.	FEATURES	SOURCE	
ORGANISM	Homo sapiens	BASE COUNT	/organism="unknown"	6 a 10 c 8 g 7 t
SOURCE		ORIGIN		
BASE COUNT	6 a 10 c 8 g 7 t			
ORIGIN				
RESULT	4		RESULT	7
AR137971			AR137971	
LOCUS	AR137971	Score 12; DB 6; Length 28;	LOCUS	AR137971
DEFINITION	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	Score 12; DB 6; Length 28;	DEFINITION	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
ACCESSION	1 (bases 1 to 130)	linear	ACCESSION	1 (bases 1 to 130)
VERSION	Cereb,N., Kong,Y., Lee,S., Maye,P. and Yang,S.Y.	PAT 16-JUN-2001	VERSION	Cereb,N., Kong,Y., Lee,S., Maye,P. and Yang,S.Y.
KEYWORDS		JOURNAL	KEYWORDS	
SOURCE		FEATURES	SOURCE	
ORGANISM		BASE COUNT	/organism="unknown"	6 a 10 c 8 g 7 t
SOURCE		ORIGIN		
BASE COUNT	6 a 10 c 8 g 7 t			
ORIGIN				

ACCESSION AM244726 VERSION AM244726.1 GI:15859605

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 234)

AUTHORS Vogel, G. and Wood, L.S.

TITLE G Protein-coupled receptors

JOURNAL Patent: WO 0166750-A 55 13-SEP-2001;

FEATURES Location/Qualifiers

source

PHARMACIA & UPJOHN COMPANY (US)

BASE COUNT 56 a 64 c 65 g 49 t

ORIGIN

Query Match Best Local Similarity 100.0%; Score 12; DB 6; Length 234; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcctctgggg 12

Db 100 GCCTCTGGGG 111

RESULT 10

LOCUS G65279 DEFINITION FBNI-64new Random genomic STS Homo sapiens STS genomic, sequence ACCESSION G65279 VERSION G65279.1 GI:921115

KEYWORDS STS.

SOURCE

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 256) tagged site.

AUTHORS Oefner, P.J.

TITLE Human random genomic STS survey, unpublished data

JOURNAL

COMMENT

Contact: Peter Oefner
Stanford Genome Center
855 California Ave., Palo Alto, CA 94304, USA
Tel: 6508121926
Fax: 6508121975

Email: oefner@genome.stanford.edu

Primer A: CCTACCTCTCCATCTCTAA

Primer B: ACAGGAGACATCGGAGAACTAAC

STS size: 265

PCR profile:

Initial denaturing step of 95 degrees C for 10 min to activate AmpliTaq Gold (1 min for AmpliTaq);

14 cycles of touchdown: 94 degrees C for 20 sec, annealing for 1 min at 63

degrees C to 56 degrees C using decrements of 0.5 degrees C, extension at 72 min;

20 cycles at 94 degrees C for 20s, 56 degrees C for 45 sec, 72 degrees C for 1 min.

Protocol:

Primer: 50 ng

Taq Polymerase: each 0.2 uM

source

Query Match Best Local Similarity 100.0%; Score 12; DB 11; Length 266; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcctctgggg 12

Db 145 GCCTCTGGGG 134

RESULT 11

LOCUS HSNL1243D DEFINITION H.sapiens genomic DNA (chromosome 3; clone NL1243D). ACCESSION X87899 VERSION X87899.1 GI:1418839

KEYWORDS

SOURCE

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 278)

AUTHORS Zabavsky, E.R.

JOURNAL Unpublished

REFERENCE

AUTHORS 2 (bases 1 to 278)

Zabavsky, E.R.

TITLE Direct Submission

JOURNAL Submitted (03-MAY-1995) Zabavsky E.R., Microbiology and Tumorbiology Center, Karolinska Institute, P.O. Box 280, Stockholm, S-171 77, SWEDEN

Location/Qualifiers

FEATURES

source

1. .278

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="3 (human)"

/cell_line="mouse/human microcell hybrid line MHC 903.1"

/clone_lib="NotI linking library"

/clone="NL1243D"

/note="genomic DNA surrounding NotI sites"

BASE COUNT 44 a 95 c 77 g 62 t

ORIGIN

Query Match Best Local Similarity 100.0%; Score 12; DB 9; Length 278; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcctctgggg 12

Db 240 GCCTCTGGGG 251

RESULT 12

JOURNAL sequence tagged sites from the human genome
COMMENT unpublished (1994)
Submitted by: Utah Center for Human Genome Research University of
Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: stecorona.med.utch.edu
Primer A: TTGGACTCCCCAGAGCGT
Primer B: TGGCTGGGGTGTAGTT
End to Label: Primer A
PCR Profile:
Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing Extension 5 94
C 10 sec. 54 C 10 sec. 72 C 20 sec. 30
56 C 10 sec. 72 C 20 sec. Mg+: 1.00 mM
Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 1.
FEATURES
source
1. .321
/organism="Homo sapiens"
/db_xref="taxon:9606"
primer_bind
197. .215
/evidence=experimental
BASE COUNT 64 a 102 c 97 g 53 t 5 others
ORIGIN
Query Match 100.0% Score 12; DB 11; Length 321;
Best Local Similarity 100.0% Pred. No. 4e-03; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcctctggggag 12
||| ||||| |||||
Db 213 GCCTCTGGGGAG 202
RESULT 15
G71854
LOCUS G71854 330 bp DNA linear STS 08-JUN-2001
DEFINITION A0122834FM017 maize leaf DNA Zea mays STS genomic, sequence tagged
size.
ACCESSION G71854
VERSION G71854.1
KEYWORDS GI:14333539
STS.
SOURCE
ORGANISM Zea mays.
Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
REFERENCE 1 (bases 1 to 330)
AUTHORS Yang, J.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
TITLE 3', UTR sequences of maize genes
JOURNAL Unpublished
COMMENT
Contact: Schnable, P.S.
Schnable laboratory
Iowa State University
4405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: CCTCATCTATGGGTTTCAGC
Primer B: GGAGAGGCTGAATCATGG
PCR Profile:
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds
PCR cycles: 31
Thermal cycler: Perkin Elmer TC
Protocol:
Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM

Buffer: Taq Polymerase: 0.05 units/ul
Total vol: 20 ul

Buffer: MgCl2: 2 mM
KCl: 50 mM
Tris HCl: 20 mM
pH: 8.4
FEATURES
source
1. .330
/organism="Zea mays"
/strain="D811"
/db_xref="taxon:4577"
/clone_lib="maize leaf DNA"
/note="PCR products amplified from genomic DNA"
<1. >330
BASE COUNT 67 a 107 c 83 g 71 t 2 others
ORIGIN
Query Match 100.0% Score 12; DB 11; Length 330;
Best Local Similarity 100.0% Pred. No. 4e-03; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gcctctggggag 12
||| ||||| |||||
Db 80 GCCTCTGGGGAG 91
Search completed: May 10, 2002, 16:15:54
Job time: 7024 sec



GenCore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; search time 68.34 Seconds
 (without alignments)
 43.131 Million cell updates/sec

Title: US-09-761-116-1
 Perfect score: 12
 Sequence: 1 gcctctgggg 12

Scoring table: IDENTITY.NUC
 Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*

3: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*

4: /cgn2_6/ptodata/2/1na/PCUTS_COMB.seq:*

5: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	12	100.0	12	4	US-09-243-335-1	Sequence 1, Appli
2	12	100.0	28	4	US-09-243-335-41	Sequence 41, Appli
3	12	100.0	28	4	US-09-243-335-46	Sequence 46, Appli
4	12	100.0	28	4	US-09-243-335-47	Sequence 47, Appli
5	12	100.0	28	4	US-09-243-335-48	Sequence 48, Appli
6	12	100.0	200	4	US-09-243-335-3	Sequence 3, Appli
7	12	100.0	1279	1	US-08-146-010A-4	Sequence 4, Appli
8	12	100.0	1279	1	US-08-674-168-9	Sequence 9, Appli
9	12	100.0	1363	1	US-08-776-088-21	Sequence 21, Appli
10	12	100.0	1363	5	PCT-US95-9145A-21	Sequence 21, Appli
11	12	100.0	1875	3	US-09-878-474-4	Sequence 4, Appli
12	12	100.0	1938	1	US-09-278-635B-1	Sequence 4, Appli
13	12	100.0	1938	3	US-08-464-258B-1	Sequence 4, Appli
14	12	100.0	1938	3	US-08-471-961-1	Sequence 9, Appli
15	12	100.0	2374	2	US-09-466-589-5	Sequence 21, Appli
16	12	100.0	2374	2	US-08-629-636-5	Sequence 4, Appli
17	12	100.0	2374	3	US-08-467-574-5	Sequence 1, Appli
18	12	100.0	2374	4	US-09-217-945-5	Sequence 1, Appli
19	12	100.0	2540	1	US-09-446-19A-1	Sequence 1, Appli
20	12	100.0	2577	2	US-08-209-521-25	Sequence 25, Appli
21	12	100.0	2655	4	US-08-456-200B-10	Sequence 10, Appli
22	12	100.0	4837	4	US-08-456-616-1	Sequence 1, Appli
23	12	100.0	5176	4	US-09-182-024A-1	Sequence 1, Appli
24	12	100.0	5434	2	US-08-1841-349-1	Sequence 1, Appli
25	12	100.0	7032	3	US-08-149-097D-24	Sequence 24, Appli
26	12	100.0	7032	3	US-08-949-386-24	Sequence 24, Appli
27	12	100.0	7032	3	US-08-450-562-24	Sequence 24, Appli

RESULT 1
 US-09-243-335-1
 ; Sequence 1, Application US/09243335A
 ; Patent No. 6197580
 ; GENERAL INFORMATION:
 ; APPLICANT: American Home Products Corp.
 ; ATTORNEY: Duzic, Edmil
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
 ; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE.
 ; FILE REFERENCE: 0630/0E791
 ; CURRENT APPLICATION NUMBER: US/09/243, 335A
 ; CURRENT FILING DATE: 1999-02-01
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 12
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 ; OTHER INFORMATION: US-09-243-335-1

Query Match 100.0%; Score 12; DB 4; Length 12;
 Best local Similarity 100.0%; Prod. No. 2.1e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcctctgggg 12
 OQ 1 gcctctgggg 12
 DB 1 gcctctgggg 12

RESULT 2
 US-09-243-335-41
 ; Sequence 41, Application US/09243335A
 ; Patent No. 6197580
 ; GENERAL INFORMATION:
 ; APPLICANT: American Home Products Corp.
 ; ATTORNEY: Duzic, Edmil
 ; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
 ; TITLE OF INVENTION: B3-ADRENERGIC RECEPTOR GENE
 ; FILE REFERENCE: 0630/0E791
 ; CURRENT APPLICATION NUMBER: US/09/243, 335A
 ; CURRENT FILING DATE: 1999-02-01
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 41
 ; LENGTH: 28

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: 
; OTHER INFORMATION: Oligonucleotide
; US-09-243-335-41

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; 
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gcctctggag 12
Db 6 gcctctggag 17

RESULT 3
US-09-243-335-46
; Sequence 46, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: American Home Products Corp.
; APPLICANT: Duzic, Edimir
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: 
; OTHER INFORMATION: Oligonucleotide
; US-09-243-335-46

Query Match 100.0%; Score 12; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; 
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gcctctggag 12
Db 6 gcctctggag 17

RESULT 4
US-09-243-335-47
; Sequence 47, Application US/09243335A
; Patent No. 6197580
; GENERAL INFORMATION:
; APPLICANT: American Home Products Corp.
; APPLICANT: Susulic, Vedrana S.
; APPLICANT: Duzic, Edimir
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN
; FILE REFERENCE: 0630/0E791
; CURRENT APPLICATION NUMBER: US/09/243,335A
; CURRENT FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: 
; US-09-243-335-47

Query Match 100.0%; Score 12; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; 
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gcctctggag 12
Db 61 gcctctggag 72

```

RESULT 7
US-08-146-010A-4/c

Sequence 4 Application US/08146010A
Patent No. 5591577

GENERAL INFORMATION:

APPLICANT: TSUCHIYA, MAKOTO
APPLICANT: MORITA, MIKO

APPLICANT: MIWA, KIYOSHI

TITLE OF INVENTION: MOBILE GENETIC ELEMENT ORIGINATED FROM

TITLE OF INVENTION: BREVIBACTERIUM STRAIN

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/146,010A

FILING DATE: 12-NOV-1993

CLASSIFICATION:

435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 52694/92

FILING DATE: 11-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-649-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-810-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-2220

TELEFAX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1279 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Brevibacterium lactofermentum

STRAIN: AJ12036

FEATURE:

NAME/KEY: repeat_region

LOCATION: 1..14

FEATURE:

NAME/KEY: repeat_region

LOCATION: 1266..1279

US-08-146-010A-4

Query Match 100.0%; Score 12; DB 1; Length 1279;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcctctggggag 12

Db 136 GCCTCTGGGGAG 125

RESULT 8

US-08-674-168-9/c

Sequence 9 Application US/08674168

Patent No. 580414

GENERAL INFORMATION:

APPLICANT: Morigi, Mika

APPLICANT: Matsui, Hiroshi

APPLICANT: Yokozeki, Kenzo

APPLICANT: Hirano, Seiko

APPLICANT: Hayakawa, Atsushi
APPLICANT: Izui, Masako

APPLICANT: Sugimoto, Masakazu

TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING

TITLE OF INVENTION: ARTIFICIAL TRANSPOSON

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P. C.

STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/674,168

FILING DATE: 01-JUL-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-166541

FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-810-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

FILING DATE: 30-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-810-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-2220

TELEFAX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 1279 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Brevibacterium lactofermentum

STRAIN: AJ12036

FEATURE:

NAME/KEY: repeat_region

LOCATION: 1..14

FEATURE:

NAME/KEY: repeat_region

LOCATION: 1266..1279

US-08-674-168-9

Query Match 100.0%; Score 12; DB 1; Length 1279;

Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcctctggggag 12

Db 136 GCCTCTGGGGAG 125

RESULT 9

US-08-776-088-21/c

Sequence 21 Application US/08776088

Patent No. 5773579

GENERAL INFORMATION:

APPLICANT: Torczynski, Richard M.

APPLICANT: Boulton, Arthur P.

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSE: SIDNEY & AUSTIN

STREET: 1201 Elm Street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/776,088

FILING DATE: 19-JUL-95

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Eugenia S. Hansen

REGISTRATION NUMBER: 31,966

REFERENCE/DOCKET NUMBER: 10365/05011

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-981-3300

TELEFAX: 214-981-3400

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 1363 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-776-088-21

RESULT 10

Query Match 100.0%; Score 12; DB 1; Length 1363;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggctctggggag 12

Db 183 GCCTCTGGGAG 172

PCT-US95-09145A-21/C

Sequence 21, Application PC/US9509145A

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Lung Cancer Marker

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSE: RICHARDS, MEDLOCK & ANDREWS

STREET: 1201 Elm Street, Suite 4500

CITY: Dallas

STATE: TX

COUNTRY: US

ZIP: 75270-2197

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/09145A

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: John A. Harre

REGISTRATION NUMBER: 37,345

TELECOMMUNICATION INFORMATION:

TELEPHONE: 214-939-4500

TELEFAX: 214-939-4500

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 1363 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-09145A-21Query Match 100.0%; Score 12; DB 5; Length 1363;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ggctctggggag 12

Db 183 GCCTCTGGGAG 172

RESULT 11

US-08-878-474-4/C
Sequence 4, Application US/08878474
Patent No. 613232

GENERAL INFORMATION:

APPLICANT: De Robertis, Edward M

TITLE OF INVENTION: Endoerm, Cardiac and Neural Inducing

TITLE OF INVENTION: Factors

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Majestic, Parsons, Siebert & Hsue

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: U.S.A.

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/878,474

FILING DATE: 18-JUN-1997

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 60/020,150

FILING DATE: 20-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Siebert, J. Suzanne

REGISTRATION NUMBER: 28,758

REFERENCE/DOCKET NUMBER: 3100.002US1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/248-5500

TELEFAX: 415/362-5418

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 1875 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-878-474-4

RESULT 12
 US-08-278-635B-1
 Sequence 1, Application US/08278635B
 Patent No. 5683912
 GENERAL INFORMATION:
 APPLICANT: ELGOYHEN, ANA BELEN
 APPLICANT: BOULTER, JAMES R.
 APPLICANT: HEINEMANN, STEPHEN F.
 TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 CITY: SAN DIEGO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/278,635B
 FILING DATE: 21-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: REITER, STEPHEN E.
 REGISTRATION NUMBER: 31,192
 REFERENCE/DOCKET NUMBER: P41 9771
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-677-1409
 TELEFAX: 619-677-1465
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1938 base Pairs
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: ALPHA 9
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 89..1525
 US-08-278-635B-1

Query Match 100.0%; Score 12; DB 1; Length 1938;
 Best Local Similarity 100.0%; Prod. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ggctctgggg 12
 Db 878 GCCTCTGGGGAG 889

RESULT 13
 US-08-464-238B-1
 Sequence 1, Application US/08464238B
 Patent No. 6013766
 GENERAL INFORMATION:
 APPLICANT: ELGOYHEN, ANA BELEN
 APPLICANT: BOULTER, JAMES R.
 APPLICANT: HEINEMANN, STEPHEN F.
 TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 CITY: SAN DIEGO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

CORRESPONDENCE ADDRESS:
 ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
 STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 CITY: SAN DIEGO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,258B
 FILING DATE: 06/05/95
 CLASSIFICATION: 530
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/278,635
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: REITER, STEPHEN E.
 REGISTRATION NUMBER: 31,192
 REFERENCE/DOCKET NUMBER: P41 9989
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-677-1409
 TELEFAX: 619-677-1465
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1938 base Pairs
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: ALPHA 9
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 89..1525
 US-08-464-238B-1

Query Match 100.0%; Score 12; DB 3; Length 1938;
 Best Local Similarity 100.0%; Prod. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ggctctgggg 12
 Db 878 GCCTCTGGGGAG 889

RESULT 14
 US-08-71-961-1
 Sequence 1, Application US/08471961
 Patent No. 610046
 GENERAL INFORMATION:
 APPLICANT: ELGOYHEN, ANA BELEN
 APPLICANT: BOULTER, JAMES R.
 APPLICANT: HEINEMANN, STEPHEN F.
 APPLICANT: BOULTER, JAMES R.
 APPLICANT: HEINEMANN, STEPHEN F.
 APPLICANT: ELGOYHEN, ANA BELEN
 APPLICANT: BOULTER, JAMES R.
 APPLICANT: HEINEMANN, STEPHEN F.
 TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
 TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GRAY CARY WARE & FREIDENRICH
 STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
 CITY: SAN DIEGO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,961
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/278,635
 FILING DATE: 21-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: RETTER, STEPHEN E.
 REGISTRATION NUMBER: 31,192
 REFERENCE/DOCKET NUMBER: P41 9771
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-677-1409
 TELEFAX: 619-238-9999
 INFORMATION FOR SEQ ID NO: 1:
 LENGTH: 1938 base pairs
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 LENGTH: 1938 base pairs
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: ALPHA 9
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 89..1525
 ;US-08-471-961-1
 ;US-08-466-589-5

Query Match 100.0%; Score 12; DB 3; Length 1938;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 878 GCCTCTGGGAG 889

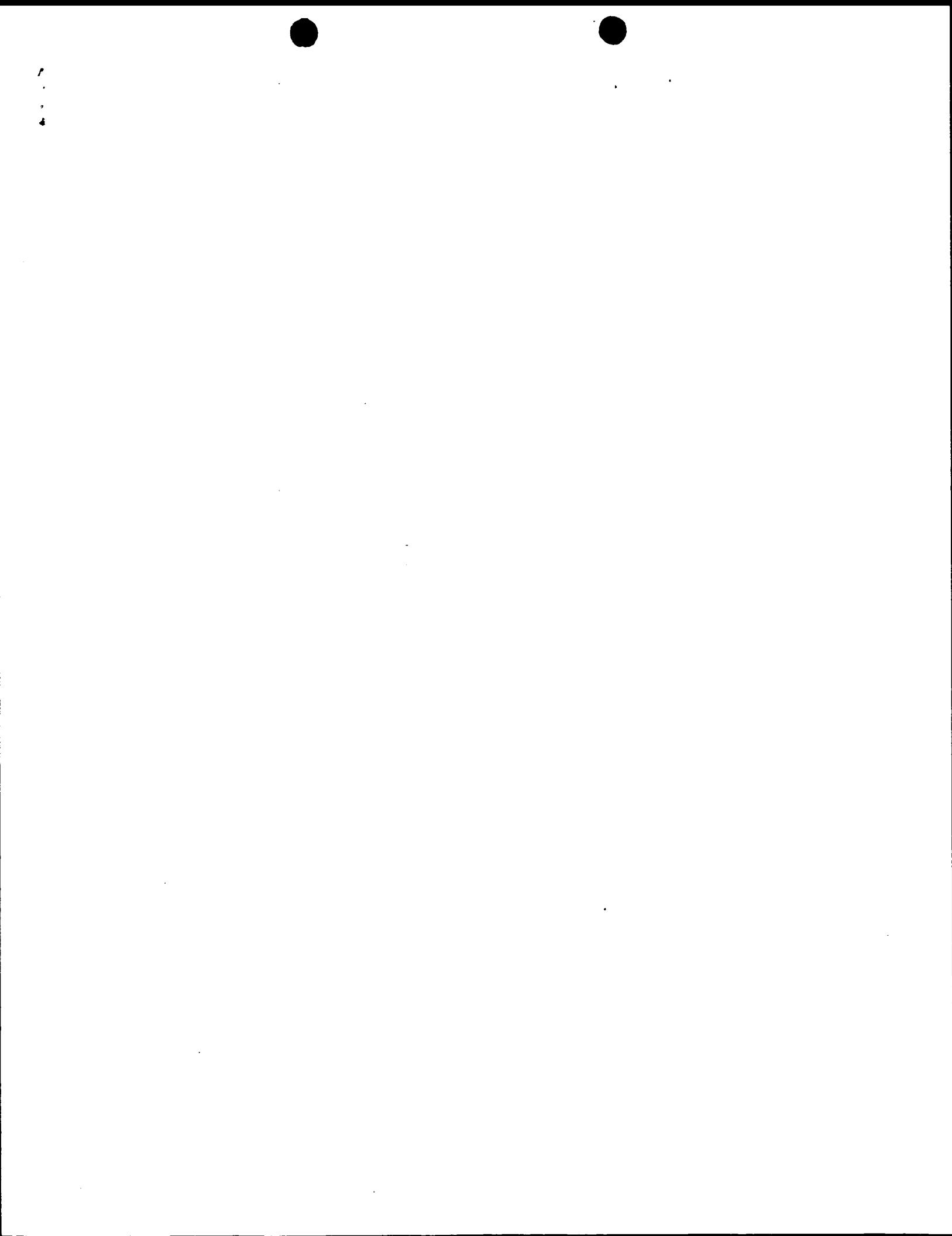
RESULT 15
 US-08-466-589-5
 Sequence 5, Application US/08466589
 Patent No. 5837489
 GENERAL INFORMATION:
 APPLICANT: Elliot, Kathryn J.
 APPLICANT: Ellis, Steven B.
 APPLICANT: Harbold, Michael M.
 TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Brown, Martin, Haller & McClain
 STREET: 1660 Union Street
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92101-3926
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/466,589
 FILING DATE: June 5, 1995
 CLASSIFICATION: 536
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: March 8, 1993

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 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;US-08-466-589-5

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 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ;US-08-466-589-5

Qy 1 gcctctggggag 12
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 Db 2237 GCCTCTGGGAG 2248

Search completed: May 10, 2002, 15:39:25
 Job time: 4835 sec



GenCore version 4.5
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On nucleic - nucleic search, using sw model

Run on: May 10, 2002, 14:18:50 ; Search time 255.59 Seconds
 (without alignments)
 80.609 Million cell updates/sec

Title: US-09-761-116-1
 Perfect score: 12
 Sequence: 1 gcctctggggag 12

Scoring table: IDENTITY-NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Minimum DB seq length: 0
 Maximum DB seq length: 0
 Maximum Match 0%

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_032802:*

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2: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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4: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1986.DAT:*

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12: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1994.DAT:*

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20: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDS1/gcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Post. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	12	100	12 21 AAA87902	Human beta-3-adren beta-3-AR segment
2	12	100	28 21 AAA87942	Beta-3-AR segment
3	12	100	28 21 AAA87947	Beta-3-AR segment
4	12	100	28 21 AAA87948	Beta-3-AR segment
5	12	100	28 21 AAA87949	Beta-3-AR segment
6	12	100	113 22 ABR76256	Human foetal liver Probe #19262 for g
7	12	100	113 22 ABR40795	Human brain express
8	12	100	113 22 AAK24907	Human bone marrow
9	12	100	113 22 AAK50902	Human bone marrow

RESULT 1
 AAA87902
 ID AAA87902 standard; DNA; 12 BP.
 AC AAA87902;
 XX DT 07-DRG-2000 (first entry)
 XX DE Human beta-3-adrenergic receptor B segment oligonucleotide SEQ ID NO:1.
 XX KW Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
 KW regulation; identification; trans-activating factor; drug screening;
 KW gene expression regulation; obesity; type II diabetes; ss.
 XX OS Homo sapiens.
 XX PN WO2000044901-A1.
 XX PD 03-AUG-2000.
 XX PF 01-FEB-2000; 2000WO-US02632.
 XX PR 01-FEB-1999; 99US-0243335.
 XX PA (AMHP) AMERICAN HOME PROD CORP.
 XX PI Sustulic VS, Duzic E;
 XX DR WPI; 2000-482973/42.
 PT New isolated nucleic acid useful for screening assays to identify
 PT compounds capable of regulating beta3-AR (adrenergic receptor)

PT expression, is composed of three regulatory segments -
 XX
 PS Claim 2: Page 57; 88pp; English.
 XX
 CC The present sequence represent the core nucleotide sequence from the
 CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
 CC trans-activating factor. Recombinant vectors under control of the
 CC transcription regulation region comprising nucleotide sequences
 CC containing the core nucleotide sequence from the B segment of the human
 CC beta-3-AR regulatory region provide a substrate for high throughput
 CC assays, particularly reporter gene assays to identify compounds capable
 CC of increasing or decreasing the level of expression of beta-3-AR. The
 CC nucleotide sequences can be used for regulating gene expression and for
 CC drug screening. It is envisaged that beta-3-AR stimulation may have
 CC beneficial effects in the treatment of obesity and type II diabetes.
 CC The present sequence represents a human beta-3-AR segment B mutational
 CC analysis oligonucleotide, which is used in the exemplification of the
 XX present invention.
 CC Sequence 28 BP; 4 A; 10 C; 8 G; 6 T; 0 other;
 CC
 SQ Sequence 12 BP; 1 A; 3 C; 6 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 21; Length 12;
 Best local similarity 100.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Qy 1 gcttcggggag 12
 Db 1 gctctggggag 12
 RESULT 2
 ID AAA87942
 ID AAA87942 standard; DNA; 28 BP.
 XX
 AC AAA87942;
 XX
 DT 07-DEC-2000 (first entry)
 XX
 DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:41.
 XX Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
 KW regulation; trans-activating factor; drug screening;
 KW gene expression regulation; obesity; type II diabetes; mutation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200044901-A1.
 XX
 PD 03-AUG-2000.
 XX
 DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:46.
 XX Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
 KW regulation; identification; trans-activating factor; drug screening;
 KW gene expression regulation; obesity; type II diabetes; mutation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200044901-A1.
 XX
 PD 03-AUG-2000.
 XX
 DE Beta-3-AR segment B mutational analysis oligonucleotide SEQ ID NO:46.
 XX Human; beta-3-adrenergic receptor; beta-3-AR; transcription; promoter;
 KW regulation; identification; trans-activating factor; drug screening;
 KW gene expression regulation; obesity; type II diabetes; mutation; ss.
 XX
 OS Homo sapiens.
 XX
 PR 01-FEB-1999; 99US-0243335.
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PT Susulic VS, Duzic E;
 XX
 DR WO200044901-A1.
 XX
 PT 01-FEB-1999; 99US-0243335.
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PT Susulic VS, Duzic E;
 XX
 DR WO200044901-A1.
 XX
 PT 01-FEB-1999; 99US-0243335.
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PT Susulic VS, Duzic E;
 XX
 DR WPI; 2000-482973/42.
 XX
 PT New isolated nucleic acid useful for screening assays to identify
 PT compounds capable of regulating beta-3-AR (adrenergic receptor)
 PT expression, is composed of three regulatory segments -
 XX
 PS Example 1; Fig 7; 88pp; English.
 XX
 CC The present invention describes a core nucleotide sequence from the
 CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
 CC region. The core nucleotide sequence binds to a B-segment-binding
 CC trans-activating factor. Recombinant vectors under control of the
 CC transcription regulation region comprising nucleotide sequences
 CC containing the core nucleotide sequence from the B segment of the human
 CC beta-3-AR regulatory region provide a substrate for high throughput
 CC assays, particularly reporter gene assays to identify compounds capable
 CC of increasing or decreasing the level of expression of beta-3-AR. The
 CC nucleotide sequences can be used for regulating gene expression and for
 CC drug screening. It is envisaged that beta-3-AR stimulation may have
 CC beneficial effects in the treatment of obesity and type II diabetes.
 CC The present sequence represents a human beta-3-AR segment B mutational
 CC analysis oligonucleotide, which is used in the exemplification of the
 CC present invention.
 XX Sequence 28 BP; 3 A; 10 C; 8 G; 7 T; 0 other;

PT expression, is composed of three regulatory segments -
 XX
 PS Claim 2: Page 57; 88pp; English.
 XX
 CC The present invention describes a core nucleotide sequence from the
 CC B segment of the human beta-3-adrenergic receptor (beta-3-AR) regulatory
 CC trans-activating factor. Recombinant vectors under control of the
 CC transcription regulation region comprising nucleotide sequences
 CC containing the core nucleotide sequence from the B segment of the human
 CC beta-3-AR regulatory region provide a substrate for high throughput
 CC assays, particularly reporter gene assays to identify compounds capable
 CC of increasing or decreasing the level of expression of beta-3-AR. The
 CC nucleotide sequences can be used for regulating gene expression and for
 CC drug screening. It is envisaged that beta-3-AR stimulation may have
 CC beneficial effects in the treatment of obesity and type II diabetes.
 CC The present sequence represents a human beta-3-AR segment B mutational
 CC analysis oligonucleotide, which is used in the exemplification of the
 CC present invention.
 XX Sequence 28 BP; 3 A; 10 C; 8 G; 7 T; 0 other;

XX
DE Human foetal liver single exon nucleic acid probe #24561.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
XX
OS Homo sapiens.
XX WO200157277-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00569.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0508408.
XX PR 03-AUG-2000; 2000US-0632466.
XX PR 21-SEP-2000; 2000US-0234887.
XX PR 27-SEP-2000; 2000US-0236559.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483447/52.
XX PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human fetal liver -
XX Claim 4; SEQ ID NO 24561; 639pp + sequence listing; English.
XX The invention relates to a single exon nucleic acid probe for
CC measuring human gene expression in a sample derived from human foetal
CC liver. The single exon nucleic acid probes may be used for predicting,
CC measuring and displaying gene expression in samples derived from human
CC fetal liver. The present sequence is a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC from WIPO at ftp://wipo.int/pub/published_pct_sequences.
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;
XX Query Match 100.0%; Score 12; DB 22; Length 113;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 gcctctggggag 12
XX ||||||| 101
XX 94 gcctctggggag 105
XX RESULT 7
XX ABR40796
XX ID ABR40796 standard; DNA; 113 BP.
XX AC ABR40796;
XX DT 23-JAN-2002 (first entry)
XX DE Probe #19262 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00667.
XX PR 04-FEB-2000; 2000US-0180312.
XX PR 26-MAY-2000; 2000US-0207456.
XX PR 30-JUN-2000; 2000US-0508408.
XX PR 03-AUG-2000; 2000US-0632466.
XX PR 21-SEP-2000; 2000US-0234887.
XX PR 27-SEP-2000; 2000US-0236559.
XX PR 04-OCT-2000; 2000GB-0024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX PS Claim 4; SEQ ID NO 19262; 530pp; English.
XX The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart. The
CC present sequence is one such probe. The probes may be used for
CC predicting, measuring and displaying gene expression in samples derived
CC from the human heart via microarrays. By measuring gene expression, the
CC probes are useful for predicting, diagnosing, grading, staging,
CC monitoring and prognosis diseases of the human heart and vascular system
CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC congenital heart disease.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp://wipo.int/pub/published_pct_sequences.
XX Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;
XX Query Match 100.0%; Score 12; DB 22; Length 113;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 gcctctggggag 12
XX ||||||| 101
XX 94 gcctctggggag 105
XX RESULT 8
XX ID AAK24907
XX AC AAK24907;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 24898.
XX KW Human; brain expressed exon; gene expression analysis; Probe;
KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
KW epilepsy; cancer; ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US00667.

PR	21-SEP-2000; 2000US-0224687.	PS	Example 4; SEQ ID NO: 25459; 658pp + Sequence Listing; English.
PR	27-SEP-2000; 2000US-0236359.	XX	The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
XX	04-OCT-2000; 2000GB-0024263.	CC	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	CC	
XX	Penn SG, Hanzel DK, Chen W, Rank DR;	CC	
DR	WPI; 2001-403446/52.	CC	
XX	Single exon nucleic acid probes for analyzing gene expression in human brain -	CC	
PT		CC	
XX	Single exon nucleic acid probes for analyzing gene expression in human brain -	CC	
PS		CC	
XX	Example 4; SEQ ID NO: 24898; 650pp + Sequence Listing; English.	CC	
CC	The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.	CC	
CC	Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;	CC	
SQ		CC	
Query Match	100.0%; Score 12; DB 22; Length 113;	CC	
Best Local Similarity	100.0%; Pred. No. 1.5e+03;	CC	
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
OY	1 gcctctgggag 12	CC	
Db	94 gcctctgggag 105	CC	
RESULT	9	CC	
ID	AAK50902 standard; DNA; 113 BP.	CC	
XX		CC	
AAK50902;		CC	
AC		CC	
XX		CC	
DT	06-NOV-2001 (first entry)	CC	
XX		CC	
DE	Human bone marrow expressed single exon probe SEQ ID NO: 25459.	CC	
XX		CC	
KW	Human; bone marrow; expressed; exon; gene expression analysis; probe;	CC	
KW	microarray; cancer; leukaemia; lymphoma; myeloma; ss.	CC	
XX		CC	
OS	Homo sapiens.	CC	
XX		CC	
PN	WO20015276-A2.	CC	
XX		CC	
PD	09-AUG-2001.	CC	
XX		CC	
PF	30-JAN-2001; 2001WO-US00670.	CC	
XX		CC	
PR	04-FEB-2000; 2000US-0180312.	CC	
XX		CC	
PR	26-MAY-2000; 2000US-020456.	CC	
PR	30-JUN-2000; 2000US-0608408.	CC	
PR	03-AUG-2000; 2000US-062323.	CC	
PR	21-SEP-2000; 2000US-0234687.	CC	
PR	27-SEP-2000; 2000US-0236359.	CC	
PR	04-OCT-2000; 2000GB-0024263.	CC	
XX		CC	
PA	(MOLE-) MOLECULAR DYNAMICS INC.	CC	
XX		CC	
PI	Penn SG, Hanzel DK, Chen W, Rank DR;	CC	
XX		CC	
DR	WPI; 2001-488901/53.	CC	
XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -	CC	
XX		CC	
PS	Claim 25; SEQ ID NO 1873; 487pp; English.	CC	
XX		CC	
CC	The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.	CC	
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences .	CC	
XX	Sequence 113 BP; 7 A; 44 C; 29 G; 33 T; 0 other;	CC	
XX		CC	
XX	WPI; 2001-488900/53.	CC	
XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -	CC	
XX		CC	

Query Match	100.0%	Score 12;	DB 22;	Length 113;	RESULT 12
Best Local Similarity	100.0%	Pred. No. 1.5e+03;			AAC15250/C
Matches	12;	Conservative	0;	Mismatches	ID AAC15250 standard; cDNA: 227 BP.
Y	1	gacctctgggg 12			XX
b	94	gacctctgggg 105			AC AAC15250;
T	07-DEC-2000	(first entry)			XX DT 06-OCT-2000 (first entry)
X					XX DE Human secreted protein 5' EST, SEQ ID NO: 19325.
E					XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
X					XX KW gene therapy; chromosome mapping; ss.
D					XX OS Homo sapiens.
C					XX PN EP1033401-A2.
W					XX PD 06-SEP-2000.
W					XX PF 21-FEB-2000; 2000EP-0200610.
X					XX PR 26-FEB-1999; 99US-0122487.
S					XX PA (GBST) GENSET.
X					XX DR WPI: 2000-500381/45.
X					XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
X					PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
X					PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
X					XX PS Claim 1; SEQ ID 19325; 71PP + CD-ROM; English.
X					XX CC The present sequence is one of a large number of 5' ESTs derived from
X					CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
X					CC identified within the present sequence. The 5' ESTs were prepared from
X					CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
X					CC sequences usually correspond mainly to the 3' untranslated region (UTR)
X					CC of the mRNA because they are often obtained from Oligo-dT primed cDNA
X					CC libraries. Such ESTs are not well suited for isolating cDNA sequences
X					CC derived from the 5' ends of mRNAs and even in those cases where longer
X					CC cDNA sequences have been obtained the full 5' UTR is rarely included.
X					CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
X					CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
X					CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
X					CC They are used to obtain upstream regulatory sequences and to design
SQ					XX expression and secretion vectors.
Qy	1	gacctctgggg 12			XX Sequence 227 BP; 50 A; 53 C; 67 G; 53 T; 4 other;
Db	169	GCCTCTGGGAG 158			XX
RESULT 13					Query Match 100.0%; Score 12; DB 21; Length 227;
AS30782					Best Local Similarity 100.0%; Pred. No. 1.5e+03;
ID					Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX					AC AAC30782;
XX					XX DT 04-DEC-2001 (first entry)
XX					XX DE Human cDNA encoding G protein-coupled receptor nGPCR-83.

XX	Human: G protein-coupled receptor; ngPCR-x; ss; antiviral; analgesic; cytostatic; cardiant; antidiabetic; anoretic; hypotensive; hypertensive; antiarkinian; nootropic; neuroprotective; antidepressant; viral infection; HIV-2; human immunodeficiency virus; HIV-2; pain; cancer; metabolic disease; cardiovascular disease; type 2 diabetes; obesity; anorexia; hypertension; myoclonic; myocardial infarction; atherosclerosis; Parkinson's disease; psychosis; neurological disorder; schizophrenia; migraine; major depression; anxiety; mental disorder; manic depression; dyskinesia; Huntington's disease; Tourette's Syndrome
XX	Homo sapiens.
XX	OS
XX	PN
XX	W020166750-A2.
PD	13-SEP-2001.
PP	08-MAR-2001: 2001WO-US07322.
PK	08-MAR-2000: 2000US-0187581.
PR	08-MAR-2000: 2000US-0187582.
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PR	08-MAR-2000: 2000US-01877825.
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PR	08-MAR-2000: 2000US-0187833.
PR	08-MAR-2000: 2000US-0187874.
PR	08-MAR-2000: 2000US-0187930.
PR	08-MAR-2000: 2000US-0188049.
PR	08-MAR-2000: 2000US-0188294.
PR	08-MAR-2000: 2000US-0187929.
PR	08-MAR-2000: 2000US-0187928.
XX	PA (PHAA) PHARMACIA & UPJOHN CO.
XX	PI vogeli G, Wood LS;
XX	DR WPI: 2001-536778/59.
DR	P-PSDB; AAU19213.
XX	Isolated nucleic acid molecules encoding G protein-coupled receptors termed ngPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and schizophrenia).
XX	Isolated nucleic acid molecules encoding G protein-coupled receptors termed ngPCR-x, useful in the treatment and diagnosis of viral infections, cancers and mental disorders (e.g. Parkinson's disease and schizophrenia).
PS	Claim 4: Page 201: 336pp; English.
XX	The invention relates to novel isolated nucleic acid molecules encoding G protein-coupled receptors termed ngPCR-x. ngPCR-x poly nucleotides, polypeptides, and modulators may be used in the treatment of diseases & conditions such as infections such as viral infections caused by HIV-1 and (human immunodeficiency virus) or HIV-2, pain, cancers, metabolic and cardiovascular diseases and disorders (e.g., type 2 diabetes, obesity, anorexia, hypertension, myocardial infarction, atherosclerosis), Parkinson's disease, and psychiatric and neurological disorders, including schizophrenia, migraine, major depression, anxiety, mental disorder, manic depression, and dyskinesias, such as Huntington's disease or Tourette's Syndrome and many other diseases and syndromes listed in the specification. ngPCR-x polynucleotides and polypeptides, as well as ngPCR-x modulators, may also be used in diagnostic assays for such diseases or conditions. The present sequence encodes a G protein-coupled receptor of the invention.
XX	Sequence 234 BP; 56 A; 64 C; 65 G; 49 T; 0 other;
SQ	

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Matches	12;										
Conservative	0;										
Mismatches	0;										
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PR	11-AUG-1999;	99US-0148171.	PR	28-OCT-1999;	99US-0161920.	PR	11-AUG-1999;	99US-0148171.	PR	28-OCT-1999;	99US-0161920.
PR	12-AUG-1999;	99US-0148341.	PR	28-OCT-1999;	99US-0161993.	PR	12-AUG-1999;	99US-0148341.	PR	28-OCT-1999;	99US-0161993.
PR	13-AUG-1999;	99US-0148565.	PR	29-OCT-1999;	99US-0162142.	PR	13-AUG-1999;	99US-0148565.	PR	29-OCT-1999;	99US-0162142.

ID ABAS1365 standard; DNA; 305 BP.
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 AC
 XX ABAS1365;
 AC
 DT 01-FEB-2002 (first entry)
 XX
 DE Human breast cell single exon nucleic acid probe #10060.
 XX
 KW Human; microarray; single exon probe; gene expression; breast;
 KW disease; cancer; ss.
 XX
 OS
 XX
 Homo sapiens.
 XX
 WO200157271-A2.
 XX
 PN
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 PF 30-JAN-2001; 2001WO-US00562.
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 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234887.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
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 DR
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 WPI; 2001-496933/54.
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 PT
 PT New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
 PT
 XX
 PS Claim 4; SEQ ID NO 10060; 327pp + sequence listing; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosis breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences.
 CC
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 SQ Sequence 305 BP; 90 A; 67 C; 110 G; 38 T; 0 other;
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 Query Match 100.0%; Score 12; DB 22; Length 305;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 gcctctggggag 12
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 Db 22 GCCTCTGGGGAG 11

Mon May 13 08:57:59 2002

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